

OIEPE

RAW SEQUENCE LISTING

DATE: 06/08/2001

PATENT APPLICATION: US/09/863,824

TIME: 17:02:30

Input Set : A:\LEX181 SEQ LIST.txt

Output Set: N:\CRF3\06082001\I863824.raw

ENTERED

4 <110> APPLICANT: Turner, C. Alexander Jr.
 5 Hilbun, Erin
 6 Donoho, Gregory
 7 Friedrich, Glenn
 8 Abuin, Alejandro
 9 Zambrowicz, Brian
 10 Sands, Arthur T.
 12 <120> TITLE OF INVENTION: Novel Human Thrombospondin-Like Proteins and Polynucleotides
 Encoding
 13 the Same
 15 <130> FILE REFERENCE: LEX-0181-USA
 C--> 17 <140> CURRENT APPLICATION NUMBER: US/09/863,824
 C--> 17 <141> CURRENT FILING DATE: 2001-05-23
 17 <150> PRIOR APPLICATION NUMBER: US 60/206,415
 18 <151> PRIOR FILING DATE: 2000-05-23
 20 <160> NUMBER OF SEQ ID NOS: 6
 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1395
 26 <212> TYPE: DNA
 27 <213> ORGANISM: homo sapiens
 29 <400> SEQUENCE: 1
 30 atggtgcgcc tggcggccga gctgctgctg ctgctggggc tgctgctgct cacgctgcac 60
 31 atcacctgtc tgcgcggctc gggagccgcc gacgggcccgc acgcggccgc gggcaacgcc 120
 32 agccaagccc agctgcagaa taacctcaac gtgggaagtgc acaccacatc agaaaccagc 180
 33 ttttctctct ccaaagaagc accaaggagc catctggacc accaggctgc acaccaaccc 240
 34 ttccccagac cgcgattccg acaagagacg gggcaccctt cattgcaaag agatttcccc 300
 35 agatcccttc tccttgatct accaaacttt ccagatcttt ccaaagtga tatcaatggg 360
 36 cagrwccaa atatccaggt caccatagag gtggtcgacg gtcctgactc tgaagcagat 420
 37 aaagatcagc atccggagaa taagcccagc ttggtcagtc catccccga ctggcgggcc 480
 38 tgggtggcaga ggtccctgtc cttggccagg gcaaacagcg gggaccagga ctacragtac 540
 39 gacagtacct cagacgacag caacttcctc aaccccccca gggggtggga ccatacagcc 600
 40 ccaggccacc ggacttttga aaccaaagat cagccagaat atgattccac agatggcgag 660
 41 ggtgactgga gtctctggtc tgtctgcagc gtcacctgcg ggaacggcaa ccagaaacgg 720
 42 acccggctct gtggctacgc gtgactgca acagaatcga ggacctgtga ccgtccaaac 780
 43 tgcccaggaa ttgaagacac ttttaggaca gctgccaccg aagtgagtct gcttgcgagg 840
 44 agcgaggagt ttaatgccac caaactgtt gaagttgaca cagacagctg tgagcgctgg 900
 45 atgagctgca aaagcgagtt cttaaagaag tacatgcaca aggtgatgaa tgacctgccc 960
 46 agctgcccct gctcctaccc cactgagggt gcctacagca cggccgacat cttcgaccgc 1020
 47 atcaagcgca aggacttccg ctggaaggac gccagcgggc ccaaggagaa gctggagatc 1080
 48 tacaagccca ctgcccggta ctgcatccgc tccatgctgt ccctggagag caccacgctg 1140
 49 gcggcacagc actgctgcta cggcgacaac atgcagctca tcaccagggg caagggggcg 1200
 50 ggcacgccc aacctcatcag cacegagttc tccgcggagc tccactaaa ggtggacgtc 1260
 51 ctgccctgga ttatctgcaa gggtgactgg agcaggtata acgaggcccc gcctcccaac 1320
 52 aacggacaga agtgcacaga gagcccctcg gacgaggact acatcaagca gttccaagag 1380
 53 gccagggaat attaa
 55 <210> SEQ ID NO: 2
 56 <211> LENGTH: 464

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57 <212> TYPE: PRT

58 <213> ORGANISM: homo sapiens

60 <220> FEATURE:

61 <221> NAME/KEY: VARIANT

62 <222> LOCATION: (1)...(464) /

63 <223> OTHER INFORMATION: Xaa = Any Amino Acid

65 <400> SEQUENCE: 2

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66 Met Val Arg Leu Ala Ala Glu Leu Leu Leu Leu Gly Leu Leu Leu
67 1 5 10 15
68 Leu Thr Leu His Ile Thr Val Leu Arg Gly Ser Gly Ala Ala Asp Gly
69 20 25 30
70 Pro Asp Ala Ala Ala Gly Asn Ala Ser Gln Ala Gln Leu Gln Asn Asn
71 35 40 45
72 Leu Asn Val Gly Ser Asp Thr Thr Ser Glu Thr Ser Phe Ser Leu Ser
73 50 55 60
74 Lys Glu Ala Pro Arg Glu His Leu Asp His Gln Ala Ala His Gln Pro
75 65 70 75 80
76 Phe Pro Arg Pro Arg Phe Arg Gln Glu Thr Gly His Pro Ser Leu Gln
77 85 90 95
78 Arg Asp Phe Pro Arg Ser Phe Leu Leu Asp Leu Pro Asn Phe Pro Asp
79 100 105 110
W--> 80 Leu Ser Lys Ala Asp Ile Asn Gly Gln Xaa Pro Asn Ile Gln Val Thr
81 115 120 125
82 Ile Glu Val Val Asp Gly Pro Asp Ser Glu Ala Asp Lys Asp Gln His
83 130 135 140
84 Pro Glu Asn Lys Pro Ser Trp Ser Val Pro Ser Pro Asp Trp Arg Ala
85 145 150 155 160
86 Trp Trp Gln Arg Ser Leu Ser Leu Ala Arg Ala Asn Ser Gly Asp Gln
87 165 170 175
W--> 88 Asp Tyr Xaa Tyr Asp Ser Thr Ser Asp Asp Ser Asn Phe Leu Asn Pro
89 180 185 190
90 Pro Arg Gly Trp Asp His Thr Ala Pro Gly His Arg Thr Phe Glu Thr
91 195 200 205
92 Lys Asp Gln Pro Glu Tyr Asp Ser Thr Asp Gly Glu Gly Asp Trp Ser
93 210 215 220
94 Leu Trp Ser Val Cys Ser Val Thr Cys Gly Asn Gly Asn Gln Lys Arg
95 225 230 235 240
96 Thr Arg Ser Cys Gly Tyr Ala Cys Thr Ala Thr Glu Ser Arg Thr Cys
97 245 250 255
98 Asp Arg Pro Asn Cys Pro Gly Ile Glu Asp Thr Phe Arg Thr Ala Ala
99 260 265 270
100 Thr Glu Val Ser Leu Leu Ala Gly Ser Glu Glu Phe Asn Ala Thr Lys
101 275 280 285
102 Leu Phe Glu Val Asp Thr Asp Ser Cys Glu Arg Trp Met Ser Cys Lys
103 290 295 300
104 Ser Glu Phe Leu Lys Lys Tyr Met His Lys Val Met Asn Asp Leu Pro
105 305 310 315 320
106 Ser Cys Pro Cys Ser Tyr Pro Thr Glu Val Ala Tyr Ser Thr Ala Asp
107 325 330 335

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```

108 Ile Phe Asp Arg Ile Lys Arg Lys Asp Phe Arg Trp Lys Asp Ala Ser
109           340           345           350
110 Gly Pro Lys Glu Lys Leu Glu Ile Tyr Lys Pro Thr Ala Arg Tyr Cys
111           355           360           365
112 Ile Arg Ser Met Leu Ser Leu Glu Ser Thr Thr Leu Ala Ala Gln His
113           370           375           380
114 Cys Cys Tyr Gly Asp Asn Met Gln Leu Ile Thr Arg Gly Lys Gly Ala
115 385           390           395           400
116 Gly Thr Pro Asn Leu Ile Ser Thr Glu Phe Ser Ala Glu Leu His Tyr
117           405           410           415
118 Lys Val Asp Val Leu Pro Trp Ile Ile Cys Lys Gly Asp Trp Ser Arg
119           420           425           430
120 Tyr Asn Glu Ala Arg Pro Pro Asn Asn Gly Gln Lys Cys Thr Glu Ser
121           435           440           445
122 Pro Ser Asp Glu Asp Tyr Ile Lys Gln Phe Gln Glu Ala Arg Glu Tyr
123           450           455           460

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125 <210> SEQ ID NO: 3

126 <211> LENGTH: 495

127 <212> TYPE: DNA

128 <213> ORGANISM: homo sapiens

130 <400> SEQUENCE: 3

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131 atgagctgca aaagcgagtt cttaaagaag tacatgcaca aggtgatgaa tgacctgccc      60
132 agctgcccct gctcctaccc cactgaggtg gcctacagca cggccgacat cttcgaccgc      120
133 atcaagcgca aggacttccg ctggaaggac gccagcgggc ccaaggagaa gctggagatc      180
134 tacaagccca ctgcccggta ctgcatccgc tccatgctgt ccctggagag caccacgctg      240
135 gcggcacagc actgctgcta cggcgacaac atgcagctca tcaccagggg caagggggcg      300
136 ggcacgcccc acctcatcag caccgagttc tccgcggagc tccactacaa ggtggacgtc      360
137 ctgccctgga ttatctgcaa gggtgactgg agcaggtata acgaggcccc gcctcccaac      420
138 aacggacaga agtgacaga gagcccctcg gacgaggact acatcaagca gttccaagag      480
139 gccagggaat attaa                                     495

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141 <210> SEQ ID NO: 4

142 <211> LENGTH: 164

143 <212> TYPE: PRT

144 <213> ORGANISM: homo sapiens

146 <400> SEQUENCE: 4

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147 Met Ser Cys Lys Ser Glu Phe Leu Lys Lys Tyr Met His Lys Val Met
148 1           5           10           15
149 Asn Asp Leu Pro Ser Cys Pro Cys Ser Tyr Pro Thr Glu Val Ala Tyr
150           20           25           30
151 Ser Thr Ala Asp Ile Phe Asp Arg Ile Lys Arg Lys Asp Phe Arg Trp
152           35           40           45
153 Lys Asp Ala Ser Gly Pro Lys Glu Lys Leu Glu Ile Tyr Lys Pro Thr
154           50           55           60
155 Ala Arg Tyr Cys Ile Arg Ser Met Leu Ser Leu Glu Ser Thr Thr Leu
156 65           70           75           80
157 Ala Ala Gln His Cys Cys Tyr Gly Asp Asn Met Gln Leu Ile Thr Arg
158           85           90           95
159 Gly Lys Gly Ala Gly Thr Pro Asn Leu Ile Ser Thr Glu Phe Ser Ala
160           100           105           110

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```

161 Glu Leu His Tyr Lys Val Asp Val Leu Pro Trp Ile Ile Cys Lys Gly
162          115          120          125
163 Asp Trp Ser Arg Tyr Asn Glu Ala Arg Pro Pro Asn Asn Gly Gln Lys
164      130          135          140
165 Cys Thr Glu Ser Pro Ser Asp Glu Asp Tyr Ile Lys Gln Phe Gln Glu
166 145          150          155          160
167 Ala Arg Glu Tyr
170 <210> SEQ ID NO: 5
171 <211> LENGTH: 936
172 <212> TYPE: DNA
173 <213> ORGANISM: homo sapiens
175 <400> SEQUENCE: 5
176 atggtgcgcc tggcggccga gctgctgctg ctgctggggc tgctgctgct cacgctgcac      60
177 atcaccgtgc tgcgcggctc gggagccgcc gacggggccg acgcggccgc gggcaacgcc      120
178 agccaagccc agctgcagaa taacctcaac gtgggaagtg acaccacatc agaaaccagc      180
179 ttttctctct ccaaagaagc accaagggag catctggacc accaggctgc acaccaaccc      240
180 ttccccagac cgcgattccg acaagagacg gggcaccctt cattgcaaag agatttcccc      300
181 agatcctttc tccttgatct accaaacttt ccagatcttt ccaaagctga tatcaatggg      360
182 cagrwttcaa atatccaggt caccatagag gtggtcgacg gtctgactc tgaagcagat      420
183 aaagatcagc atccggagaa taagcccagc tggtcagtcc catccccga ctggcggggc      480
184 tggtagcaga ggtccctgtc cttggccagg gcaaacagcg gggaccagga ctacragtac      540
185 gacagtacat cagacgacag caacttcctc aaccccccca gggggtggga ccatacagcc      600
186 ccaggccacc ggacttttga aaccaaagat cagccagaat atgattccac agatggcgag      660
187 ggtgactgga gtctctggtc tgtctgcagc gtcacctgcg ggaacggcaa ccagaaacgg      720
188 acccggtctt gtggctacgc gtgactgca acagaatcga ggacctgtga ccgtccaaac      780
189 tgcccaggaa ttgaagacac ttttaggaca gctgccaccg aagtgagtct gcttgcgggg      840
190 agcgaggagt ttaatgccac caaactgttt gaagttgtgc tcccagcatg tgtcttgctt      900
191 gctgaatata cttcaagcaa gagaaaacag tcctaa      936
193 <210> SEQ ID NO: 6
194 <211> LENGTH: 311
195 <212> TYPE: PRT
196 <213> ORGANISM: homo sapiens
198 <220> FEATURE:
199 <221> NAME/KEY: VARIANT
200 <222> LOCATION: (1)...(311) /
201 <223> OTHER INFORMATION: Xaa = Any Amino Acid
203 <400> SEQUENCE: 6
204 Met Val Arg Leu Ala Ala Glu Leu Leu Leu Leu Gly Leu Leu Leu
205 1          5          10          15
206 Leu Thr Leu His Ile Thr Val Leu Arg Gly Ser Gly Ala Ala Asp Gly
207      20          25          30
208 Pro Asp Ala Ala Ala Gly Asn Ala Ser Gln Ala Gln Leu Gln Asn Asn
209      35          40          45
210 Leu Asn Val Gly Ser Asp Thr Thr Ser Glu Thr Ser Phe Ser Leu Ser
211      50          55          60
212 Lys Glu Ala Pro Arg Glu His Leu Asp His Gln Ala Ala His Gln Pro
213 65          70          75          80
214 Phe Pro Arg Pro Arg Phe Arg Gln Glu Thr Gly His Pro Ser Leu Gln
215      85          90          95

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```

216 Arg Asp Phe Pro Arg Ser Phe Leu Leu Asp Leu Pro Asn Phe Pro Asp
217      100      105      110
W--> 218 Leu Ser Lys Ala Asp Ile Asn Gly Gln Xaa Pro Asn Ile Gln Val Thr
219      115      120      125
220 Ile Glu Val Val Asp Gly Pro Asp Ser Glu Ala Asp Lys Asp Gln His
221      130      135      140
222 Pro Glu Asn Lys Pro Ser Trp Ser Val Pro Ser Pro Asp Trp Arg Ala
223 145      150      155      160
224 Trp Trp Gln Arg Ser Leu Ser Leu Ala Arg Ala Asn Ser Gly Asp Gln
225      165      170      175
W--> 226 Asp Tyr Xaa Tyr Asp Ser Thr Ser Asp Asp Ser Asn Phe Leu Asn Pro
227      180      185      190
228 Pro Arg Gly Trp Asp His Thr Ala Pro Gly His Arg Thr Phe Glu Thr
229      195      200      205
230 Lys Asp Gln Pro Glu Tyr Asp Ser Thr Asp Gly Glu Gly Asp Trp Ser
231      210      215      220
232 Leu Trp Ser Val Cys Ser Val Thr Cys Gly Asn Gly Asn Gln Lys Arg
233 225      230      235      240
234 Thr Arg Ser Cys Gly Tyr Ala Cys Thr Ala Thr Glu Ser Arg Thr Cys
235      245      250      255
236 Asp Arg Pro Asn Cys Pro Gly Ile Glu Asp Thr Phe Arg Thr Ala Ala
237      260      265      270
238 Thr Glu Val Ser Leu Leu Ala Gly Ser Glu Glu Phe Asn Ala Thr Lys
239      275      280      285
240 Leu Phe Glu Val Val Leu Pro Ala Cys Val Leu Leu Ala Glu Tyr Thr
241      290      295      300
242 Ser Ser Lys Arg Lys Gln Ser
243 305      310

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VERIFICATION SUMMARY

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Input Set : A:\LEX181 SEQ LIST.txt

Output Set: N:\CRF3\06082001\I863824.raw

L:17 M:270 C: Current Application Number differs, Replaced Current Application No

L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:80 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2

L:88 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2

L:218 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:226 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6